Supplemental Online Content

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eAppendix 1. Code for Analysis

This supplemental material has been provided by the authors to give readers additional information about their work.

eAppendix. Code for Analysis

The analyses were run in R (r-project.org) using the following code.

```
# incubation period
p symp onset <- function(t, logmu inc=1.63, logsd inc=0.5) {
 plnorm(t, logmu_inc, logsd_inc)
# relative infectiousness over time
infectiousness daily <- function(t, t peak inf, days inf) {
 optim duration <- function(scale) {</pre>
  shape <- t peak inf / scale + 1
  abs(diff(qgamma(c(0.01, 0.99), shape=shape, scale=scale)) - days inf)
 }
 scale <- optimize(optim duration, c(0.1, 10))$minimum
 shape <- t peak inf / scale + 1
 dgamma(t, shape=shape, scale=scale)
# proportion of transmission from never symptomatic
trans_never_symp <- function(prop_never_symp, rel_inf_never_symp) {</pre>
(prop never symp * rel inf never symp) /
  (prop_never_symp * rel_inf_never_symp + (1 - prop_never_symp))
}
### Example calculations
times <- 0:100
trans never symp baseline <-
trans_never_symp(prop_never_symp=0.3, rel_inf_never_symp=0.75)
t peak inf <- 5
days inf <- 10
prop symptomatic <- (1 - trans never symp baseline) *</pre>
 sum(p inc(times) * infectious g(times, t peak inf=t peak inf, days inf=days inf))
# Never symptomatic
prop never symptomatic
# Symptomatic
prop_symptomatic
# Pre-symptomatic
1 - prop never symptomatic - prop symptomatic
```